

• = potential N-linked glycosylation sites

FIGURE 1

GGAAGTGGCTTCATTTTCAGTGGCTGACTTCCAGAGAGCAAT 41  
 ATGGCTGGTTCCCCAACATGCCTCACCTCATCTATATCCTTTGGCAGCTCACAGGGTCA 101  
 M A G S P T C L T L I Y I L W Q L T G S 20  
 GCAGCCTCTGGACCCGTGAAAGAGCTGGTCGGTTCCGTTGGTGGGGCCGTGACTTTCCCC 161  
 A A S G P V K E L V G S V G G A V T F P 40  
 CTGAAGTCCAAAGTAAAGCAAGTTGACTCTATTGTCTGGACCTTCAACACAACCCCTCTT 221  
 L K S K V K Q V D S I V W T F N T T P L 60  
 GTCACCATACAGCCAGAAGGGGGCACTATCATAGTGACCCAAAATCGTAATAGGGAGAGA 281  
 V T I Q P E G G T I I V T Q N R N R E R 80  
 GTAGACTTCCCAGATGGAGGCTACTCCCTGAAGCTCAGCAAATGAAGAAGAATGACTCA 341  
 V D F P D G G Y S L K L S K L K K N D S 100  
 GGGATCTACTATGTGGGGATATACAGCTCATCACTCCAGCAGCCCTCCACCCAGGAGTAC 401  
 G I Y Y V G I Y S S S L Q Q P S T Q E Y 120  
 GTGCTGCATGTCTACGAGCACCTGTCAAAGCCTAAAGTCACCATGGGTCTGCAGAGCAAT 461  
 V L H V Y E H L S K P K V T M G L Q S N 140  
 AAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATGGAACATGGGGAAGAGGATGTG 521  
 K N G T C V T N L T C C M E H G E E D V 160  
 ATTTATACCTGGAAGGCCCTGGGGCAAGCAGCCAAATGAGTCCCATATGGGTCCATCCTC 581  
 I Y T W K A L G Q A A N E S H N G S I L 180  
 CCCATCTCCTGGAGATGGGGAGAAAGTGATATGACCTTCATCTGCGTTGCCAGGAACCCT 641  
 P I S W R W G E S D M T F I C V A R N P 200  
 GTCAGCAGAAACTTCTCAAGCCCCATCCTTGCCAGGAAGCTCTGTGAAGGTGCTGCTGAT 701  
 V S R N E S S P I L A R K L C E G A A D 220  
 GACCCAGATTCCCTCCATGGTCCCTCTGTGCTCTCTGTTGGTGCCCTCCTGCTCAGTCTC 761  
 D P D S S M V L L C L L L V P L L L S L 240  
 TTTGTACTGGGGCTATTTCTTTGGTTTCTGAAGAGAGAGACAAGAAGAGTACATTGAA 821  
 F V L G L F L W F L K R E R Q E E Y I E 260  
 GAGAAGAAGAGAGTGGACATTTGTGGGAAACTCCTAACATATGCCCCCATTTCTGGAGAG 881  
 E K K R V D I C R E T P N I C P H S G E 280  
 AACACAGAGTACGACACAATCCCTCACACTAATAGAACAATCCTAAAGGAAGATCCAGCA 941  
 N T E Y D T I P H T N R T I L K E D P A 300  
 AATACGGTTTACTCCACTGTGGAAATACCGAAAAAGATGGAAAATCCCCACTCACTGCTC 1001  
 N T V Y S T V E I P K K M E N P H S L L 320  
 ACGATGCCAGACACACCAAGGCTATTTGCCTATGAGAATGTTATCTAGACAGCAGTGCAC 1061  
 T M P D T P R L F A Y E N V I \* 335  
 TCCCCTAAGTCTCTGCTCAAAAAAAAAACAATTCTCGGCCCAAAGAAAACAATCAGAAGA 1121  
 ATTCAGTGAATTTGACTAGAAACATCAAGGAAGAATGAAGAACGTTGACTTTTTTCCAGGA 1181  
 TAAATTATCTCTGATGCTTCTTTAGATTTAAGAGTTCGTAATTCATCCACTGCTGAGAA 1241  
 ATCTCCTCAAACCCAGAAGGTTAATCACTTCATCCAAAAATGGGATTGTGAATGTCAG 1301  
 CAAACCATAAAAAAAGTGCTTAGAAGTATTCTATAGAAATGTAAATGCAAGGTCACACA 1361  
 TATTAATGACAGCCTGTTGTATTAATGATGGCTCCAGGTGAGTGTCTGGAGTTTCATTCC 1421  
 ATCCCAGGGCTTGATGTCAGGATTATACCAAGAGTCTTGCTACCAGGAGGGCAAGAAGA 1481  
 CCAAAACAGACAGACAAGTCCAGCAGAAGCAGATGCACCTGACAAAAATGGATGTATTAA 1541  
 TTGGCTCTATAAACTATGTGCCAGCACTATGCTGAGCTTACACTAATTGGTCAGACGTG 1601  
 CTGTCTGCCCTCATGAAATGGCTCCAAATGAATGAACACTTTTCATGAGCAGTTGTAGC 1661  
 AGGCCTGACCACAGATTCCAGAGGGCCAGGTGTGGATCCACAGGACTTGAAGGTCAAAG 1721  
 TTCACAAAGATGAAGAATCAGGGTAGCTGACCATGTTTGGCAGATACTATAATGGAGACA 1781  
 CAGAAGTGTGCATGGCCCAAGGACAAGGACCTCCAGCCAGGCTTCATTTATGCACTTGTG 1841  
 CTGCAAAAGAAAAGTCTAGGTTTTAAGGCTGTGCCAGAACCCATCCCAATAAAGAGACCG 1901  
 AGTCTGAAGTCACATTGTAAATCTAGTGTAGGAGACTTGGAGTCAGGCAGTGAGACTGGT 1961  
 GGGGCACGGGGGGCAGTGGGTACTTGTAAACCTTTAAAGATGGTTAATTCATTCAATAGA 2021  
 TATTTATTAAGAACCTACTATGCGGCCCGGCATGGTGGCTCACACCTGTAATCCCAGCAC 2081  
 TTTGGGAGGCCAAGGTGGGTGGGTGCTGAGGTGAGGTTCAAGACCAGCCTGCCCAA 2141  
 CATGGTGAAACCCCATCTCTACTAAAGATCAAAATTTGCTGAGCGTGGTGGTGTGCACCT 2201

FIGURE 2

GTATCCCAGCTACTCGAGAGGCCAAGGCATGAGAATCGCTTGAACCTGGAGGTGAGGTTG 2261  
CAGTGAGCTGAGATGGCACCCTGCACTCCGGCCTAGGCAACGAGAGCAAACTCCAATA 2321  
CAAACAAACAAACAAACACCTGTGCTAGGTGAGTCTGGCACGTAAGATGAACATCCCTAC 2381  
CAACACAGAGCTCACCATCTCTTATACTTAAGTGAAAAACATGGGGAAGGGGAAGGGGA 2441  
ATGGCTGCTTTTGATATGTTCCCTGACGCATATCTTGAATGGAGACCTCCCTACCAAGTG 2501  
ATGAAAGTGTTGAAAACTTAATAACAAATGCTTGTGGGCAAGAATGGGATTGAGGATT 2561  
ATCTTCTCTCAGAAAGGCATTGTGAAGGAATTGAGCCAGATCTCTCTCCCTACTGCAAAA 2621  
CCCTATTGTAGTAAAAAAGTCTTCTTTACTATCTTAATAAAACAGATATTGTGAGATTCA 2681  
CATAAAAAAAAAAAAAAAAAAAAA

**FIGURE 2 (continued)**

CCATCCTAATACGACTCACTATAGGGCTCGAGCGGCCGCCCGGGCAGGTTTCAAGTTCCA  
 1 -----+-----+-----+-----+-----+-----+-----+  
  
 CGTTCCTACTGCTAAGAGTCTTAGCTTACAAAAGATATTCTTGTAAGCCAAGTGTGAAG  
 61 -----+-----+-----+-----+-----+-----+-----+  
  
 TTAATCACGACAACCAAAGGTTTGCTAACATAGAGGAAGAGCTCTCATCAATAGGGGAAC  
 121 -----+-----+-----+-----+-----+-----+-----+  
  
 AGAAAGTCTCAGCGACAAGCTTATGAAAGAATGGCTGTCTCAAGGGCTCCAACACCCGAC  
 181 -----+-----+-----+-----+-----+-----+-----+  
 M A V S R A P T P D  
  
 TCCGCCTGTCAGAGGATGGTCTGGCTCTTCCACTTGTCTTCTGCCTCGGCTCAGGGAGT  
 241 -----+-----+-----+-----+-----+-----+-----+  
 S A C Q R M V W L F P L V F C L G S G S  
  
 GAAGTTTCACAGAGCAGCTCAGACCCCCAGCTAATGAATGGCGTTCTAGGAGAGTCTGCA  
 301 -----+-----+-----+-----+-----+-----+-----+  
 E V S Q S S S D P Q L M N G V L G E S A  
  
 GTTCTTCCTCTAAAGCTTCCTGCAGGGAAGATAGCCAATATCATCATCTGGAATTATGAA  
 361 -----+-----+-----+-----+-----+-----+-----+  
 V L P L K L P A G K I A N I I I W N Y E  
  
 TGGGAAGCGTCACAAGTCACTGCCCTCGTTATCAACCTAAGTAATCCTGAAAGTCCACAA  
 421 -----+-----+-----+-----+-----+-----+-----+  
 W E A S Q V T A L V I N L S N P E S P Q  
  
 ATCATGAACACTGATGTAAAGAAGAGACTGAACATCACCCAGTCCTACTCCCTGCAAATC  
 481 -----+-----+-----+-----+-----+-----+-----+  
 I M N T D V K K R L N I T Q S Y S L Q I  
  
 AGCAACCTTACCATGGCAGACACAGGATCATACTGCGCAGATAACCACAAAGGACTCT  
 541 -----+-----+-----+-----+-----+-----+-----+  
 S N L T M A D T G S Y T A Q I T T K D S  
  
 GAAGTGATCACCTTCAAATATATTCTGAGGGTCTTTGAACGATTGGGTAACTTAGAAACT  
 601 -----+-----+-----+-----+-----+-----+-----+  
 E V I T F K Y I L R V F E R L G N L E T

**FIGURE 3**

661 ACCAACTATACTCTCCTGCTAGAGAATGGGACCTGCCAGATACACCTGGCCTGTGTTTTG  
 -----+-----+-----+-----+-----+-----+  
 T N Y T L L L E N G T C Q I H L A C V L

721 AAGAATCAAAGTCAAACGTCTCAGTTGAGTGGCAAGCCACAGGAAACATCTCTTTAGGA  
 -----+-----+-----+-----+-----+-----+  
 K N Q S Q T V S V E W Q A T G N I S L G

781 GGACCAAATGTCACCTATCTTTTGGGACCCGAGGAATTCTGGTGACCAGACTTACGTCTGC  
 -----+-----+-----+-----+-----+-----+  
 G P N V T I F W D P R N S G D Q T Y V C

841 AGAGCCAAGAATGCTGTCAGCAATTTGTCAGTCTCTGTTTCGACCCAGAGTCTCTGCAAA  
 -----+-----+-----+-----+-----+-----+  
 R A K N A V S N L S V S V S T Q S L C K

901 GGGGTTCTAACTAATCCACCCTGGAATGCAGTATGGTTTATGACTACAATTTCAATAATC  
 -----+-----+-----+-----+-----+-----+  
 G V L T N P P W N A V W F M T T I S I I

961 AGTGCAGTCATACTCATCTTTGTGTGCTGGAGCATACTGTTTGGGAAGAGAAGAGGTTCT  
 -----+-----+-----+-----+-----+-----+  
 S A V I L I F V C W S I H V W K R R G S

1021 CTCCTTTGACTAGCCAACATCCAGAGTCCTCCCAGAGCACAGATGGCCCAGGCTCTCCA  
 -----+-----+-----+-----+-----+-----+  
 L P L T S Q H P E S S Q S T D G P G S P

1081 GGGAACACTGTGTATGCACAAGTCACTCGTCCAATGCAGGAAATGAAAATCCCAAACCT  
 -----+-----+-----+-----+-----+-----+  
 G N T V Y A Q V T R P M Q E M K I P K P

1141 ATCAAAAATGACTCCATGACAATTTACTCCATAGTTAATCATTCAGAGAGGAAACAGTG  
 -----+-----+-----+-----+-----+-----+  
 I K N D S M T I Y S I V N H S R E E T V

1201 GCTTTAACCGGCTATAACCAACCCATTACCCTGAAGGTTAACACTTTAATCAACTATAAC  
 -----+-----+-----+-----+-----+-----+  
 A L T G Y N Q P I T L K V N T L I N Y N

1261 TCCTGAAGGAAGAGCACTGCAGTGACTTGAGGAAATTAAACAATGCTGTCACCACAGCTC  
 -----+-----+-----+-----+-----+-----+  
 S \*

**FIGURE 3 (continued)**

1321 TGGCTTAGATTAATGAAGTCAGCATCTCTGGAGATTGAGCGCTGCCATTTGCATTGTTCA  
-----+-----+-----+-----+-----+-----+  
1381 AACGCTTTCTAGGTGGTATGGTGAGATGCCAGAGGGCTAAGGGCCATTATAGCAGGGTAG  
-----+-----+-----+-----+-----+-----+  
1441 TTTGACTAGGAATACATAAGATAGAAAGCCTAGAATCGTATCATTGAAAGGGACAATGGA  
-----+-----+-----+-----+-----+-----+  
1501 CCTAAGAGAAGTGGAAATAAAATTGTGTCACACAAAAAAAAAAAAAAAAAAAAAAAAAG  
-----+-----+-----+-----+-----+-----+  
1561 CTTGT  
----- 1565

**FIGURE 3 (continued)**

# Apex-3 nucleotide with translation

```

GAATTCGAATTCGGGACTTTCCAGAAGGACCACAGCTCCTCCCGTGCATCCACTCGGCCT
1  -----+-----+-----+-----+-----+-----+-----+
GGGAGGTTCTGGATTTTGGCTGTCTGAGGGAGTTTGCCTGCCTCTCCAGAGAAAGATGGTC
61 -----+-----+-----+-----+-----+-----+-----+
                                                                M  V
ATGAGGCCCTGTGGAGTCTGCTTCTCTGGGAAGCCCTACTTCCCATTACAGTTACTGGT
121 -----+-----+-----+-----+-----+-----+-----+
M  R  P  L  W  S  L  L  L  W  E  A  L  L  P  I  T  V  T  G
GCCCAAGTGCTGAGCAAAGTCGGGGGCTCGGTGCTGCTGGTGGCAGCGCGTCCCCCTGGC
181 -----+-----+-----+-----+-----+-----+-----+
A  Q  V  L  S  K  V  G  G  S  V  L  L  V  A  A  R  P  P  G
TTCCAAGTCCGTGAGGCTATCTGGCGATCTCTCTGGCCTTCAGAAGAGCTCCTGGCCACG
241 -----+-----+-----+-----+-----+-----+-----+
F  Q  V  R  E  A  I  W  R  S  L  W  P  S  E  E  L  L  A  T
TTTTTCCGAGGCTCCCTGGAGACTCTGTACCATTCCCGCTTCCTGGGCCGAGCCCAGCTA
301 -----+-----+-----+-----+-----+-----+-----+
F  F  R  G  S  L  E  T  L  Y  H  S  R  F  L  G  R  A  Q  L
CACAGCAACCTCAGCCTGGAGCTCGGGCCGCTGGAGTCTGGAGACAGCGGCAACTTCTCC
361 -----+-----+-----+-----+-----+-----+-----+
H  S  N  L  S  L  E  L  G  P  L  E  S  G  D  S  G  N  F  S
GTGTTGATGGTGGACACAAGGGGCCAGCCCTGGACCCAGACCCTCCAGCTCAAGGTGTAC
421 -----+-----+-----+-----+-----+-----+-----+
V  L  M  V  D  T  R  G  Q  P  W  T  Q  T  L  Q  L  K  V  Y
GATGCAGTGCCCAGGCCCGTGGTACAAGTGTTTCATTGCTGTAGAAAGGGATGCTCAGCCC
481 -----+-----+-----+-----+-----+-----+-----+
D  A  V  P  R  P  V  V  Q  V  F  I  A  V  E  R  D  A  Q  P
TCCAAGACCTGCCAGGTTTCTTGTCTGTTGGGCCCCCAACATCAGCGAAATAACCTAT
541 -----+-----+-----+-----+-----+-----+-----+
S  K  T  C  Q  V  F  L  S  C  W  A  P  N  I  S  E  I  T  Y

```

FIGURE 4

601 AGCTGGCGACGGGAGACAACCATGGACTTTGGTATGGAACCACACAGCCTCTTCACAGAC  
 -----+-----+-----+-----+-----+-----+  
 S W R R E T T M D F G M E P H S L F T D

661 GGACAGGTGCTGAGCATTTCCCTGGGACCAGGAGACAGAGATGTGGCCTATTCCTGCATT  
 -----+-----+-----+-----+-----+-----+  
 G Q V L S I S L G P G D R D V A Y S C I

721 GTCTCCAACCCTGTCAGCTGGGACTTGGCCACAGTCACGCCCTGGGATAGCTGTCATCAT  
 -----+-----+-----+-----+-----+-----+  
 V S N P V S W D L A T V T P W D S C H H

781 GAGGCAGCACCAGGGAAGGCCTCCTACAAAGATGTGCTGCTGGTGGTGGTGCCTGTCTCG  
 -----+-----+-----+-----+-----+-----+  
 E A A P G K A S Y K D V L L V V V P V S

841 CTGCTCCTGATGCTGGTTACTCTCTTCTCTGCCTGGCACTGGTGCCCCTGCTCAGGGAAA  
 -----+-----+-----+-----+-----+-----+  
 L L L M L V T L F S A W H W C P C S G K

901 AAGAAAAAGGATGTCCATGCTGACAGAGTGGGTCCAGAGACAGAGAACCCCCTTGTGCAG  
 -----+-----+-----+-----+-----+-----+  
 K K K D V H A D R V G P E T E N P L V Q

961 GATCTGCCATAAAGGACAATATGAACTGATGCCTGGACTATCAGTAACCCCCTGCACAG  
 -----+-----+-----+-----+-----+-----+  
 D L P \*

1021 GCACACGATGCTCTGGGACATAACTGGTGCCTGGAAATCACCATGGTCCTCATATCTCCC  
 -----+-----+-----+-----+-----+-----+

1081 ATGGGAATCCTGTCCTGCCTCGAAGGAGCAGCCTGGGCAGCCATCACACCACGAGGACAG  
 -----+-----+-----+-----+-----+-----+

1141 GAAGCACCAGCACGTTTCACACCTCCCCCTTCCCTCTCCCATCTTCTCATATCCTGGCTC  
 -----+-----+-----+-----+-----+-----+

1201 TTCTCTGGGCAAGATGAGCCAAGCAGAACATTCCATCCAGGACACTGGAAGTTCTCCAGG  
 -----+-----+-----+-----+-----+-----+

**FIGURE 4 (continued)**







MSK NQK QG SML VS \*

AGVSE RAS PQTS PDS SAPI CQLRM NVW LFGPELS VFA CLGL  
KLP SNILRACTVISMADRTIMNTYVKWKELATGSIWNTVAKIERTLGSQIT  
NLSINLVCTVIFSLKWDQSPNCISQNTVQINVTQNLQDLSVETTWQCPVWN  
QIHLNATSIHISAEKSIQVILSPNLTYSQITGVDGWNSTPHVNTL  
SNTLTPEITQEAMLTKSIPKSPITWCFVCGPSSGSMITGNY  
RTREREETVAVSMQVLAETKSGNTPVYNNNS

FIGURE 6

M	V	M	R	P	L	W	S	L	L	L	W	E	A	L	L	P	I	T	V	T	G
A	Q	V	L	S	K	V	G	G	S	V	L	L	V	A	A	R	P	P	G	F	Q
V	R	E	A	I	W	R	S	L	W	P	S	E	E	L	L	A	T	F	R	S	G
S	L	E	T	L	Y	H	S	R	F	L	G	R	A	Q	L	H	S	N	L	R	L
E	L	G	P	L	E	S	G	D	S	G	N	F	S	V	L	M	V	D	T	Q	G
Q	P	W	T	Q	T	L	Q	L	K	V	Y	D	A	V	P	R	P	V	V	W	V
F	I	A	V	E	R	D	A	Q	P	S	K	T	C	Q	V	F	L	C	Q	E	A
P	N	I	S	E	I	T	Y	S	W	R	R	E	T	T	M	D	F	M	W	V	P
H	S	L	F	T	D	G	Q	V	L	S	I	S	L	G	P	G	R	D	E	A	C
Y	S	C	I	V	S	N	P	V	S	W	D	L	A	T	V	T	W	D	S	C	S
H	H	E	A	A	P	G	K	A	S	Y	K	D	V	L	L	V	V	P	V	S	K
L	L	L	M	L	V	T	L	F	S	A	W	H	W	C	P	C	G	K	K	K	*
K	D	V	H	A	D	R	V	G	P	E	T	E	N	P	L	V	Q	L	P		

FIGURE 7

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**FIGURE 8**

# Tissue Distribution of Apex1 Expression

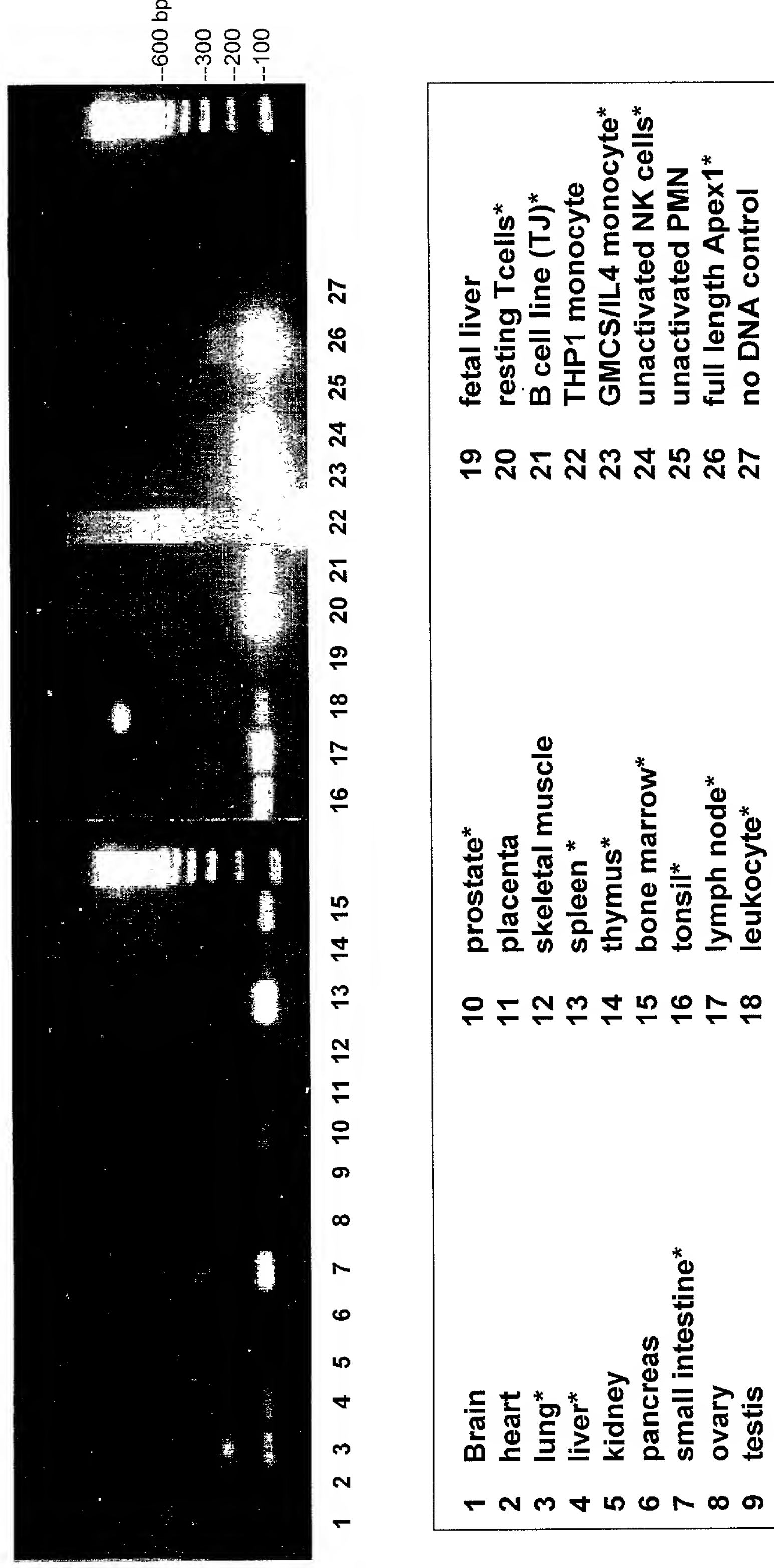


FIGURE 9

## Peptides in APEX-1Ig

**1 MAGSPTCLTL IYILWQLTGS AASGPVKELV** GSVGGA VTFP LKSKVKQVDS  
51 IVWTFNTTPL VTIQPEGGTI IVTQNRNRER VDFPDGGYSL KLSKLKKNDS  
101 GIYYVGIYSS SLQQPSTQEY VLHVYEHLSK PKVTMGLQSN KNGTCVTNLT  
151 CCMEHGEEDV IYTWKALGQA ANESHNGSIL PISWRWGESD MTFICVARNP  
201 VSRNFSSPIL ARKLCEGAAD DPDSS HP humanIgG1 H-CH2-CH3

**Bold-** Predicted signal sequence, which will be cleaved in mature protein    HP - junction sequence resulting from the BamH1 enzyme site.

**FIGURE 10**

### Peptides in APEX-2mIg

1 **MAVSRAPTPD** **SACQRMVWLF** **PLVFCLGSGS** EVSQSSSDPQ LMNGVLGESA  
51 VLPLKLPAGK IANIIIWNYE WEASQVTALV INLSNPESPQ IMNTDVKKRL  
101 NITQSYSLQI SNLTMA DTGS YTAQITTKDS EVITFKYILR VFERLGNLET  
151 TNYTLLLENG TCQIHLACVL KNQSQTVSVE WQATGNISLG GPNVTIFWDP  
201 RNSGDQTYVC RAKNAVS NLS VSVSTQSLCK GVL TNPPW HP - murine  
IgG2a H-Ch2-CH3

**Bold-** Predicted signal sequence, which will be cleaved in the mature protein    HP - junction sequence resulting from the BamH1 enzyme site.

### FIGURE 11



any, they will not open in the way they are at the top of the book. The book is not open in the way they are at the top of the book.

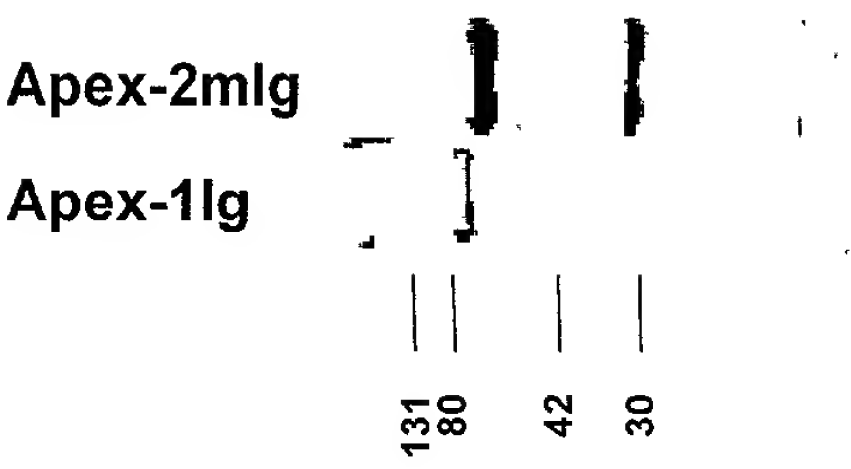
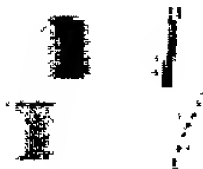


FIGURE 12

the first and second steps in the process of the invention are carried out in the presence of a catalyst.

Sf9  
Cos

148 —



60 —

**FIGURE 13**

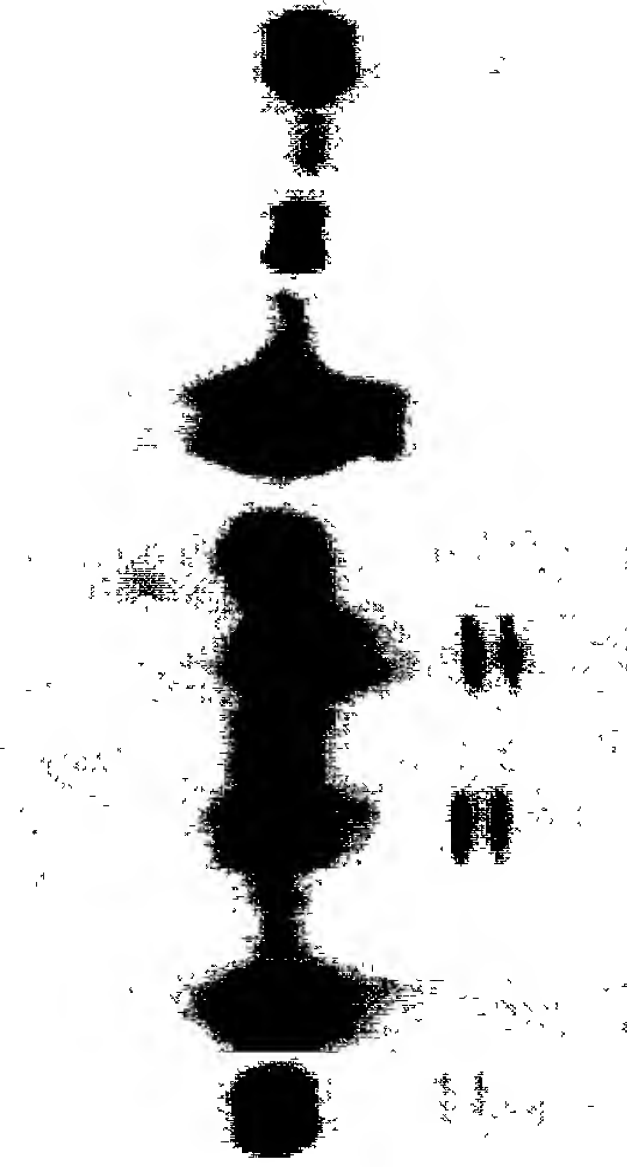
Apex1 Antibody Panel

# Apex1 Antibody Panel

Reduced

13 30 31 34 35 36 40 66 67 68 71 73

204 kb--  
121--  
78--  
40--  
30--



Non reduced

13 30 31 34 35 36 40 66 67 68 69 71 73

204--  
121--  
78--  
40--  
30--

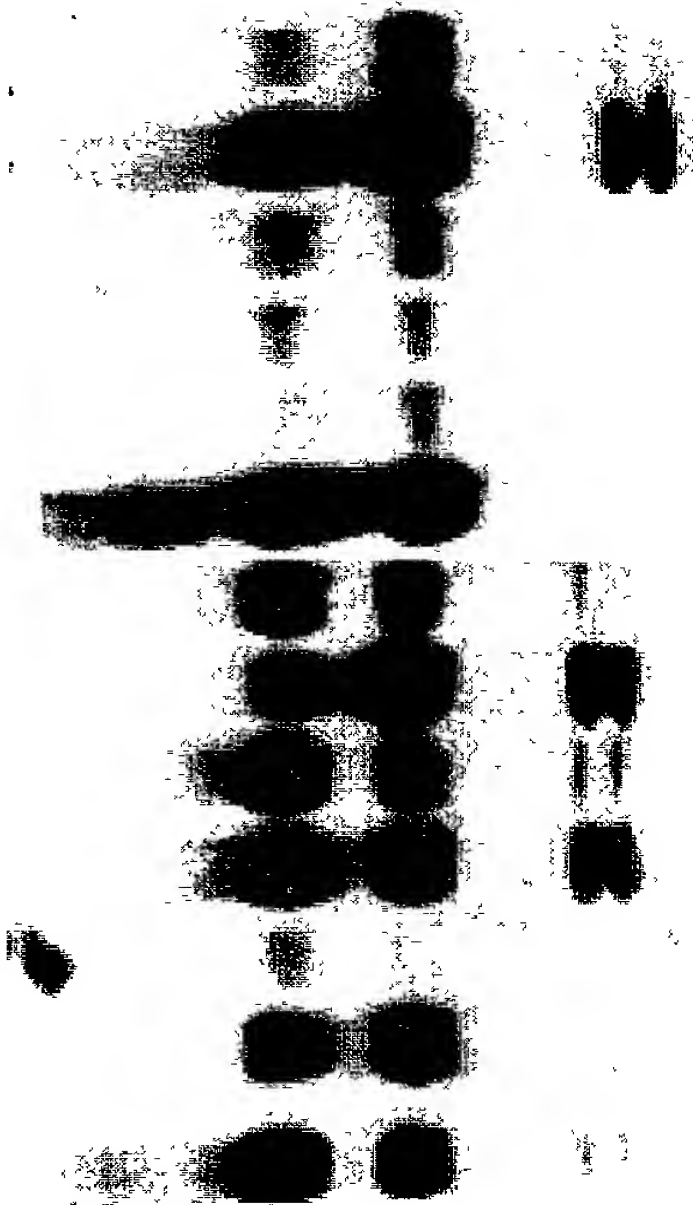


FIGURE 14

**FLAG-APEX-1**

**MPMGS**LQPLATLYLL**GMLVASCLG**DYKDDDDKSGPVKELVGSVGGAVTFP  
LKSKVKQVDSIVWTFNTTPLVTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDS  
GIYYVGIYSSSLQQPSTQEYVLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEVDV  
IYTWKALGQAANESHNGSILPISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAAD  
DPDSSMVLLCLLLVPLLLSLFVLGLFLWFLKRERQEEYIEEKKRVDICRETPNICPHSGE  
NTEYDTIPHTNRTILKEDPANTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI\*

**MPMGS**LQPLATLYLL**GMLVASCLG** sequence from human CD5 signal peptide,  
DYKDDDDK is the FLAG peptide

**FIGURE 15**

## FLAG-APEX-2

MPMGS**LQPLATLYLLGMLVASCLG**DYKDDDDKSEVSQSSSDPQLMNGVLGESA  
VLPLKLPAGKIANIIIWNYEWEASQVTALVINLSNPESPQIMNTDVKKRLNITQSYSLQI  
SNLTMADTGSYTAQITTKDSEVITFKYILRVFERLG~~N~~LETTNYTLLLENGTCQIHLACVL  
KNQSQTVSVEWQATGNISLG~~G~~PNVTIFWDPRNSGDQTYVCRAKNAVSNLSVSVSTQSLCK  
GVLTNPPWNAVWFMTTISIISAVILIFVCWSIHVWKRRGSLPLTSQHP~~E~~SSQSTDGPGSP  
GNTVYAQVTRPMQEMKIPKPIK~~N~~DSMTIYSIVNHSREETVALTGYNQPITLKVNTLINYS\*

MPMGS**LQPLATLYLLGMLVASCLG** sequence from human CD5 signal peptide,  
**DYKDDDDK** is the FLAG peptide

## FIGURE 16